



SEQUENCE LISTING

<10> Sandstrom, Paula

<120> Methods for Regulating Bud-Hypha Transitions and cAMP Levels in
Candida albicans

<130> 48544-00012 (DC-0293)

<140> US 10/672,074

<141> 2003-09-29

<150> US 09/801,774

<151> 2001-03-09

<160> 29

<170> PatentIn version 3.3

<210> 1

<211> 545

<212> PRT

<213> Candida albicans

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Thr Ile Phe Gln Glu Glu Ala Asn Lys Asn His Tyr Gly Val Asp Ser
35 40 45

Leu Thr Glu Lys Gly Thr Pro Lys Ser Arg Thr Val Glu Ser Ser Glu
50 55 60

Ala Thr Ser Asp Gly Lys Ser Leu Glu Ser Thr Ser Phe Ala Thr Phe
65 70 75 80

Ser Glu Ala Pro Val Glu Lys Ser Lys Leu Ile Val Glu Phe Glu Asn
85 90 95

Phe Val Glu Ser Tyr Val His Pro Leu Val Glu Thr Ser Lys Lys Ile
100 105 110

Asp Ser Leu Val Gly Glu Ser Ala Gln Tyr Phe Tyr Glu Ala Phe Val
115 120 125

Glu Gln Gly Lys Phe Leu Glu Leu Val Leu Gln Ser Gln Gln Pro Asp
130 135 140

Met Thr Asp Pro Ala Leu Ala Lys Ala Leu Glu Pro Met Asn Ala Lys
145 150 155 160

Cys Thr Lys Ile Asn Glu Leu Lys Asp Ser Asn Arg Lys Ser Pro Phe
165 170 175

Phe Asn His Leu Ser Thr Phe Ser Glu Ser Asn Ala Val Phe Tyr Trp
180 185 190

Ile Gly Ile Pro Thr Pro Val Ser Tyr Ile Thr Asp Thr Lys Asp Thr
195 200 205

Val Lys Phe Trp Ser Asp Arg Val Leu Lys Glu Tyr Lys Thr Lys Asp
210 215 220

Gln Val His Val Glu Trp Val Lys Gln Thr Leu Ser Val Phe Asp Glu
225 230 235 240

Leu Lys Asn Tyr Val Lys Glu Tyr His Thr Thr Gly Val Ala Trp Asn
245 250 255

Pro Lys Gly Lys Pro Phe Ala Glu Val Val Ser Gln Gln Thr Glu Ser
260 265 270

Ala Ala Lys Asn Ser Ser Ser Ala Ser Gly Ser Ala Gly Gly Ala Ala
275 280 285

Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Thr Phe Phe Asp Asp Thr
290 295 300

Glu Lys Asp Ser Glu Asn Pro Ser Pro Ala Ser Gly Gly Ile Asn Ala
305 310 315 320

Val Phe Ala Glu Leu Asn Gln Gly Ala Asn Ile Thr Ser Gly Leu Lys
325 330 335

Lys Val Asp Lys Ser Glu Met Thr His Lys Asn Pro Glu Leu Arg Lys
340 345 350

Gln Pro Pro Val Ala Pro Lys Lys Pro Ala Pro Pro Lys Lys Pro Ser
355 360 365

Ser Leu Ser Gly Gly Val Ser Ser Ala Pro Val Lys Lys Pro Ala Lys
370 375 380

Lys Glu Leu Ile Asp Gly Thr Lys Trp Ile Ile Gln Asn Phe Thr Lys
385 390 395 400

Ala Asp Ile Ser Asp Leu Ser Pro Ile Thr Ile Glu Val Glu Met His
405 410 415

Gln Ser Val Phe Ile Gly Asn Cys Ser Asp Val Thr Ile Gln Leu Lys
420 425 430

Gly Lys Ala Asn Ala Val Ser Val Ser Glu Thr Lys Asn Val Ala Leu
435 440 445

Val Ile Asp Ser Leu Ile Ser Gly Val Asp Val Ile Lys Ser Tyr Lys
450 455 460

Phe Gly Ile Gln Val Leu Gly Leu Val Pro Met Leu Ser Ile Asp Lys
465 470 475 480

Ser Asp Glu Gly Thr Ile Tyr Leu Ser Gln Glu Ser Ile Asp Asn Asp
485 490 495

Ser Gln Val Phe Thr Ser Ser Thr Thr Ala Leu Asn Ile Asn Ala Pro
500 505 510

Lys Glu Asn Asp Asp Tyr Glu Glu Leu Ala Val Pro Glu Gln Phe Val
515 520 525

Ser Lys Val Val Asn Gly Lys Leu Val Thr Gln Ile Val Glu His Ala
530 535 540

Gly
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<213> Candida albicans

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aatcgtcaga agcaacttcc gatggtaaatt cactcgaatc tacatcattt gccacttttt 240
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gcacccaaat taacgaatta aaaattccaa tcgtaaatct ccattcttca atcattttaag 540
cactttcagt gaaagtaatg ccgtttttta ttggattggg atccctacac cagtctcgta 600
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gaccaaagac caagtgcatt ttgaatgggt aaaacaaaca ttatctgttt ttgacgaatt 720
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gtagcactac agcactcaac atcaatgcac caaaggaaaa tgatgattat gaagaattgg 1560
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 <213> Candida albicans

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20

25

30

Pro Thr Ala Leu Leu Tyr Asn Asp Arg Ser Val Leu Glu Ser Tyr His
35 40 45

Ala Ser Leu Phe Ile Asn Lys Val Leu Arg Ile Cys Trp Pro Asp Leu
50 55 60

Leu Thr Cys Thr Ile Glu Glu Lys Ser Glu Leu Thr Ile Arg Ser Leu
65 70 75 80

Ile Ile Ser Ser Ile Leu Ala Thr Asp Met Gly Glu His Asn Glu Tyr
85 90 95

Val Asn Arg Leu Lys Ser Phe Lys Thr His Asn Glu Ile Leu Asn His
100 105 110

Asp Asn Thr Val Lys Leu Ile Ser Ala Leu Leu Ile Lys Cys Ala Asp
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Ile Ser Asn Val Thr Arg Pro Leu Arg Val Ser Ala Gln Trp Ala Met
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Val Leu Ser Arg Glu Phe
145 150

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<213> *Saccharomyces cerevisiae*

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20 25 30

Glu Val Ala Gln Asn Phe Lys Asn Val Ser Ile Leu Glu Asn Phe His
35 40 45

Arg Glu Leu Phe Gln Gln Leu Leu Ser Glu His Trp Pro Gln Leu Leu
50 55 60

Ser Ile Ser Lys Lys Lys Phe Asp Phe Ile Ser Glu Ala Ile Leu Ala
65 70 75 80

Thr Asp Met Ala Leu His Ser Gln Tyr Glu Asp Arg Leu Met His Glu
85 90 95

Asn Pro Met Lys Gln Ile Thr Leu Ile Ser Leu Ile Ile Lys Ala Ala
100 105 110

Asp Ile Ser Asn Val Thr Arg Thr Leu Ser Ile Ser Ala Arg Trp Ala
115 120 125

Tyr Leu Ile Thr Leu Glu Phe
130 135

<210> 5

<211> 149

<212> PRT

<213> Homo sapiens

<400> 5

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Leu Asp His Arg Gly Thr Asn Asn Ser Phe Gln Val Ala Ser Lys Ser
20 25 30

Val Leu Ala Ala Leu Tyr Ser Ser Glu Gly Ser Val Met Glu Arg His
35 40 45

His Phe Ala Gln Ala Ile Ala Ile Leu Asn Thr His Gly Cys Asn Ile
50 55 60

Phe Asp His Phe Ser Arg Lys Asp Tyr Gln Arg Met Leu Asp Leu Met
65 70 75 80

Arg Asp Ile Ile Leu Ala Thr Asp Leu Ala His His Leu Arg Ile Phe
85 90 95

Lys Asp Leu Gln Lys Met Ala Glu Val Gly Tyr Asp Arg Asn Asn Lys
100 105 110

Gln His His Arg Leu Leu Leu Cys Leu Leu Met Thr Ser Cys Asp Leu
115 120 125

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Ile Tyr Lys Glu Phe
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<220>
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22

<210> 7
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide

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20

<210> 8
<211> 566
<212> PRT
<213> Candida albicans

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20 25 30

Phe Lys Lys Thr Ser Thr Glu Thr Asp Ser Asn Val Pro Ile Val Ile
35 40 45

Ile Phe Pro Thr Asn Asn Asp Ile Pro Ser Arg Lys Thr Arg Ser Thr
50 55 60

Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Asn Thr Ser Lys Leu Asp
65 70 75 80

Asn Leu Pro Phe Ser Asp Lys Ser Leu Leu Ile Gln Phe Phe Phe Thr
85 90 95

His Leu Asn Ile Leu Met Ile Gln Gly Glu Asn Ser Asp Glu Gly Lys
100 105 110

Leu Tyr Gln Glu Ile Ser Ser Ala Lys Glu Leu Leu Thr Asn Arg Ile
115 120 125

Ser Arg Val Gly Asn Trp Thr Gly Thr Thr His Phe Arg Tyr Cys Arg
130 135 140

His Glu Asn Asp Cys Gly Leu Leu Asn Gln His Ser Lys Ile Ala Gly
145 150 155 160

Ile Ile Pro Thr Met Thr Tyr Ile Leu Asn Cys Asn Ala Thr Arg Ser
165 170 175

Glu Ile Ala Thr Asn Gln Leu Ile Tyr Leu Tyr Arg Leu Met Ile Glu
180 185 190

Glu Ile Asn Phe Ile Glu Leu Leu Gln Asp Ala Ser Thr Thr Arg Leu
195 200 205

Ser Gln Leu Cys Tyr Ala Val Gly His Trp Ser Phe Pro Ala His Asn
210 215 220

Leu Ser Asn Asp Asp Leu Val Tyr Cys Val Tyr Leu Met Ile Asp Tyr
225 230 235 240

Ala Ile Lys Gln Val Glu Gly Phe Asp Asn Ile Pro Leu Asn Glu Leu
245 250 255

Leu Ala Phe Ile Phe Ile Val Arg Asp Thr Tyr Lys Asn Gly Asn Pro
260 265 270

Phe His Asn Phe Arg His Ala Val Asp Val Leu Gln Ala Cys Phe His
275 280 285

Phe Leu Ile Arg Leu Gly Ser Leu Pro Lys Phe Lys Gln Phe Val Glu
290 295 300

Asp Pro Lys Leu Asp Tyr Thr Glu Val His Asp Thr His Thr Val Leu
305 310 315 320

Ile Ala Leu Gln Asn Asn Ser Ser Glu Glu Lys Ala Ser Leu Asn Pro
325 330 335

Ile Gln Thr Leu Gly Leu Leu Val Ala Ala Leu Gly His Asp Val Gly
340 345 350

His Pro Gly Thr Thr Asn Asp Phe Met Ile Lys Phe Ser Ala Pro Thr
355 360 365

Ala Leu Leu Tyr Asn Asp Arg Ser Val Leu Glu Ser Tyr His Ala Ser
370 375 380

Leu Phe Ile Asn Lys Val Leu Arg Ile Cys Trp Pro Asp Leu Leu Thr
385 390 395 400

Cys Thr Ile Glu Glu Lys Ser Glu Leu Thr Ile Arg Ser Leu Ile Ile
405 410 415

Ser Ser Ile Leu Ala Thr Asp Met Gly Glu His Asn Glu Tyr Val Asn
420 425 430

Arg Leu Lys Ser Phe Lys Thr His Asn Glu Ile Leu Asn His Asp Asn
435 440 445

Thr Val Lys Leu Ile Ser Ala Leu Leu Ile Lys Cys Ala Asp Ile Ser
450 455 460

Asn Val Thr Arg Pro Leu Arg Val Ser Ala Gln Trp Ala Met Val Leu
465 470 475 480

Ser Arg Glu Phe Ala Glu Val Glu Leu Leu Lys Ser Val Ile Lys Lys
485 490 495

Asp Ile Asp Leu Asp Phe Thr Lys Asp Leu Thr Tyr Asp Asp Val Pro
500 505 510

His Glu Leu Arg Glu Ile Leu Glu Ile Gln Pro Asp Ile His Lys Gly
515 520 525

Gln Ile Phe Phe Ile Asn Leu Phe Ala Glu Asn Leu Phe Asn Ser Val
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Asn Lys Leu Phe Trp Leu
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<212> PRT
<213> Candida albicans

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Asp Lys Tyr Tyr Lys Phe Asp Thr Phe Lys His Leu Ile Cys His Leu
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Phe Lys Lys Thr Ser Thr Glu Thr Asp Ser Asn Val Pro Ile Val Ile
35 40 45

Ile Phe Pro Thr Asn Asn Asp Ile Pro Ser Arg Lys Thr Arg Ser Thr
50 55 60

Thr Thr Thr Thr Thr Thr Ala Thr Thr Thr Asn Thr Ser Lys Leu Asp
65 70 75 80

Asn Leu Pro Phe Ser Asp Lys Ser Leu Leu Ile Gln Phe Phe Phe Thr
85 90 95

His Leu Asn Ile Leu Met Ile Gln Gly Glu Asn Ser Asp Glu Gly Lys
100 105 110

Leu Tyr Gln Glu Ile Ser Ser Ala Lys Glu Leu Leu Thr Asn Arg Ile
115 120 125

Ser Arg Val Gly Asn Trp Thr Gly Thr Thr His Phe Arg Tyr Cys Arg
130 135 140

His Glu Asn Asp Cys Gly Leu Leu Asn Gln His Ser Lys Ile Ala Gly
145 150 155 160

Ile Ile Pro Thr Met Thr Tyr Ile Leu Asn Cys Asn Ala Thr Arg Ser
165 170 175

Glu Ile Ala Thr Asn Gln Leu Ile Tyr Leu Tyr Arg Leu Met Ile Glu
180 185 190

Glu Ile Asn Phe Ile Glu Leu Leu Gln Asp Ala Ser Thr Thr Arg Leu
195 200 205

Ser Gln Leu Cys Tyr Ala Val Gly His Trp Ser Phe Pro Ala His Asn
210 215 220

Leu Ser Asn Asp Asp Leu Val Tyr Cys Val Tyr Leu Met Ile Asp Tyr
225 230 235 240

Ala Ile Lys Gln Val Glu Gly Phe Asp Asn Ile Pro Leu Asn Glu Leu
245 250 255

Leu Ala Phe Ile Phe Ile Val Arg Asp Thr Tyr Lys Asn Gly Asn Pro
260 265 270

Phe His Asn Phe Arg His Ala Val Asp Val Leu Gln Ala Cys Phe His
275 280 285

Phe Leu Ile Arg Leu Gly Ser Leu Pro Lys Phe Lys Gln Phe Val Glu
290 295 300

Asp Pro Lys Leu Asp Tyr Thr Glu Val His Asp Lys His Thr Val Leu
305 310 315 320

Ile Ala Leu Gln Asn Asn Ser Ser Glu Glu Lys Ala Ser Leu Asn Pro
325 330 335

Ile Gln Thr Leu Gly Leu Leu Val Ala Ala Leu Gly His Asp Val Gly
340 345 350

His Pro Gly Thr Thr Asn Asp Phe Met Ile Lys Phe Ser Ala Pro Thr
355 360 365

Ala Leu Leu Tyr Asn Asp Arg Ser Val Leu Glu Ser Tyr His Ala Ser
370 375 380

Leu Phe Ile Asn Lys Val Leu Arg Ile Cys Trp Pro Asp Leu Leu Thr
385 390 395 400

Cys Thr Ile Glu Glu Lys Ser Glu Leu Thr Ile Arg Ser Leu Ile Ile
405 410 415

Ser Ser Ile Leu Ala Thr Asp Met Gly Glu His Asn Glu Tyr Val Asn
420 425 430

Arg Leu Lys Ser Phe Lys Thr His Asn Glu Ile Leu Asn His Asp Asn
435 440 445

- 12 -

Thr Val Lys Leu Ile Ser Ala Leu Leu Ile Lys Cys Ala Asp Ile Ser
450 455 460

Asn Val Thr Arg Pro Leu Arg Val Ser Ala Gln Trp Ala Met Val Leu
465 470 475 480

Ser Arg Glu Phe Ala Glu Val Glu Leu Leu Lys Ser Val Ile Lys Lys
485 490 495

Asp Ile Asp Leu Asp Phe Thr Lys Asp Leu Thr Tyr Asp His Val Pro
500 505 510

His Glu Leu Arg Glu Ile Leu Glu Ile Gln Pro Asp Ile His Lys Gly
515 520 525

Gln Ile Phe Phe Ile Asn Leu Phe Ala Glu Asn Leu Phe Asn Ser Val
530 535 540

Ser Asp Leu Leu Pro Gln Leu Gln Tyr Thr Cys Asp Ile Ile Met Glu
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Asn Lys Leu Phe Trp Leu Glu Arg Ala Lys Lys
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23

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 12

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<210> 13

<211> 1716

<212> DNA

<213> *Candida albicans*

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gattcaaatg ttcctatagt aataatattc ccgaccaaca atgatatccc ttcgagaaaag	180
actcgatcta ctactaccac caccaccact actactacta ctaataccag caagttagac	240
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<220>
<223> Synthetic oligonucleotide

<400> 14
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<220>
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<400> 15
ggctggtaga gacttgacca accatttg 28

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<213> Saccharomyces cerevisiae

<400> 16

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35 40 45

Lys Pro Ser Asp Ser Gly Ala Asp Ala Asn Thr Thr Asn Glu Pro Ser
50 55 60

- 15 -

Ala Glu Asn Ala Pro Glu Val Glu Gln Asp Pro Lys Cys Ile Thr Ala
65 70 75 80

Phe Gln Ser Tyr Ile Gly Glu Asn Ile Asp Pro Leu Val Glu Leu Ser
85 90 95

Gly Lys Ile Asp Thr Val Val Leu Asp Ala Leu Gln Leu Leu Lys Gly
100 105 110

Gly Phe Gln Ser Gln Leu Thr Phe Leu Arg Ala Ala Val Arg Ser Arg
115 120 125

Lys Pro Asp Tyr Ser Ser Gln Thr Phe Ala Asp Ser Leu Arg Pro Ile
130 135 140

Asn Glu Asn Ile Ile Lys Leu Gly Gln Leu Lys Glu Ser Asn Arg Gln
145 150 155 160

Ser Lys Tyr Phe Ala Tyr Leu Ser Ala Leu Ser Glu Gly Ala Pro Leu
165 170 175

Phe Ser Trp Val Ala Val Asp Thr Pro Val Ser Met Val Thr Asp Phe
180 185 190

Lys Asp Ala Ala Gln Phe Trp Thr Asn Arg Ile Leu Lys Glu Tyr Arg
195 200 205

Glu Ser Asp Pro Asn Ala Val Glu Trp Val Lys Lys Phe Leu Ala Ser
210 215 220

Phe Asp Asn Leu Lys Ala Tyr Ile Lys Glu Tyr His Thr Thr Gly Val
225 230 235 240

Ser Trp Lys Lys Asp Gly Met Asp Phe Ala Asp Ala Met Ala Gln Ser
245 250 255

Thr Lys Asn Thr Gly Ala Thr Ser Ser Pro Ser Pro Ala Ser Ala Thr
260 265 270

Ala Ala Pro Ala Pro Pro Pro Pro Pro Ala Pro Pro Ala Ser Val
275 280 285

Phe Glu Ile Ser Asn Asp Thr Pro Ala Thr Ser Ser Asp Ala Asn Lys
290 295 300

- 16 -

Gly Gly Ile Gly Ala Val Phe Ala Glu Leu Asn Gln Gly Glu Asn Ile
305 310 315 320

Thr Lys Gly Leu Lys Lys Val Asp Lys Ser Gln Gln Thr His Lys Asn
325 330 335

Pro Glu Leu Arg Gln Ser Ser Thr Val Ser Ser Thr Gly Ser Lys Ser
340 345 350

Gly Pro Pro Pro Arg Pro Lys Lys Pro Ser Thr Leu Lys Thr Lys Arg
355 360 365

Pro Pro Arg Lys Glu Leu Val Gly Asn Lys Trp Phe Ile Glu Asn Tyr
370 375 380

Glu Asn Glu Thr Glu Ser Leu Val Ile Asp Ala Asn Lys Asp Glu Ser
385 390 395 400

Ile Phe Ile Gly Lys Cys Ser Gln Val Leu Val Gln Ile Lys Gly Lys
405 410 415

Val Asn Ala Ile Ser Leu Ser Glu Thr Glu Ser Cys Ser Val Val Leu
420 425 430

Asp Ser Ser Ile Ser Gly Met Asp Val Ile Lys Ser Asn Lys Phe Gly
435 440 445

Ile Gln Val Asn His Ser Leu Pro Gln Ile Ser Ile Asp Lys Ser Asp
450 455 460

Gly Gly Asn Ile Tyr Leu Ser Lys Glu Ser Leu Asn Thr Glu Ile Tyr
465 470 475 480

Thr Ser Cys Ser Thr Ala Ile Asn Val Asn Leu Pro Ile Gly Glu Asp
485 490 495

Asp Asp Tyr Val Glu Phe Pro Ile Pro Glu Gln Met Lys His Ser Phe
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Ala Asp Gly Lys Phe Lys Ser Ala Val Phe Glu His Ala Gly
515 520 525

<210> 17
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<213> Schizosaccharomyces pombe

<400> 17

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50 55 60

Ala Pro Thr Val Ser Thr Gly Ser Pro Ala Val Ala Ser Leu His Asp
65 70 75 80

Gln Val Ala Ala Ala Ile Ser Pro Arg Asn Arg Ser Leu Thr Ser Thr
85 90 95

Ser Ala Val Glu Ala Val Pro Ala Ser Ile Ser Ala Tyr Asp Glu Phe
100 105 110

Cys Ser Lys Tyr Leu Ser Lys Tyr Met Glu Leu Ser Lys Lys Ile Gly
115 120 125

Gly Leu Ile Ala Glu Gln Ser Glu His Val Glu Lys Ala Phe Asn Leu
130 135 140

Leu Arg Gln Val Leu Ser Val Ala Leu Lys Ala Gln Lys Pro Asp Met
145 150 155 160

Asp Ser Pro Glu Leu Leu Glu Phe Leu Lys Pro Ile Gln Ser Glu Leu
165 170 175

Leu Thr Ile Thr Asn Ile Arg Asp Glu His Arg Thr Ala Pro Glu Phe
180 185 190

Asn Gln Leu Ser Thr Val Met Ser Gly Ile Ser Ile Leu Gly Trp Val
195 200 205

Thr Val Glu Pro Thr Pro Leu Ser Phe Met Ser Glu Met Lys Asp Ser
210 215 220

- 18 -

Ser Gln Phe Tyr Ala Asn Arg Val Met Lys Glu Phe Lys Gly Lys Asp
225 230 235 240

Asp Leu Gln Ile Glu Trp Val Arg Ser Tyr Leu Thr Leu Leu Thr Glu
245 250 255

Leu Ile Thr Tyr Val Lys Thr His Phe Lys Thr Gly Leu Thr Trp Ser
260 265 270

Thr Lys Gln Asp Ala Val Pro Leu Lys Thr Ala Leu Ala Asn Leu Ser
275 280 285

Ala Ser Lys Thr Gln Ala Pro Ser Ser Gly Asp Ser Ala Asn Gly Gly
290 295 300

Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Asn Asp Phe Trp Lys
305 310 315 320

Asp Ser Asn Glu Pro Ala Pro Ala Asp Asn Lys Gly Asp Met Gly Ala
325 330 335

Val Phe Ala Glu Ile Asn Lys Gly Glu Gly Ile Thr Ser Gly Leu Arg
340 345 350

Lys Val Asp Lys Ser Glu Met Thr His Lys Asn Pro Asn Leu Arg Lys
355 360 365

Thr Gly Pro Thr Pro Gly Pro Lys Pro Lys Ile Lys Ser Ser Ala Pro
370 375 380

Ser Lys Pro Ala Glu Thr Ala Pro Val Lys Pro Pro Arg Ile Glu Leu
385 390 395 400

Glu Asn Thr Lys Trp Phe Val Glu Asn Gln Val Asp Asn His Ser Ile
405 410 415

Val Leu Asp Ser Val Glu Leu Asn His Ser Val Gln Ile Phe Gly Cys
420 425 430

Ser Asn Cys Thr Ile Ile Ile Lys Gly Lys Leu Asn Thr Val Ser Met
435 440 445

Ser Asn Cys Lys Arg Thr Ser Val Val Val Asp Thr Leu Val Ala Ala
450 455 460

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Phe Asp Ile Ala Lys Cys Ser Asn Phe Gly Cys Gln Val Met Asn His
465 470 475 480

Val Pro Met Ile Val Ile Asp Gln Cys Asp Gly Gly Ser Ile Tyr Leu
485 490 495

Ser Lys Ser Ser Leu Ser Ser Glu Val Val Thr Ser Lys Ser Thr Ser
500 505 510

Leu Asn Ile Asn Val Pro Asn Glu Glu Gly Asp Tyr Ala Glu Arg Ala
515 520 525

Val Pro Glu Gln Ile Lys His Lys Val Asn Glu Lys Gly Glu Leu Val
530 535 540

Ser Glu Ile Val Arg His Glu
545 550

<210> 18
<211> 474
<212> PRT
<213> Mus musculus

<400> 18

Met Ala Asp Met Gln Asn Leu Val Glu Arg Leu Glu Arg Ala Val Gly
1 5 10 15

Arg Leu Glu Ala Val Ser His Thr Ser Asp Met His Cys Gly Tyr Gly
20 25 30

Asp Ser Pro Ser Lys Gly Ala Val Pro Tyr Val Gln Ala Phe Asp Ser
35 40 45

Leu Leu Ala Asn Pro Val Ala Glu Tyr Leu Lys Met Ser Lys Glu Ile
50 55 60

Gly Gly Asp Val Gln Lys His Ala Glu Met Val His Thr Gly Leu Lys
65 70 75 80

Leu Glu Arg Ala Leu Leu Ala Thr Ala Ser Gln Cys Gln Gln Pro Ala
85 90 95

Gly Asn Lys Leu Ser Asp Leu Leu Ala Pro Ile Ser Glu Gln Ile Gln
100 105 110

Glu	Val	Ile	Thr	Phe	Arg	Glu	Lys	Asn	Arg	Gly	Ser	Lys	Phe	Phe	Asn	115	120	125
His	Leu	Ser	Ala	Val	Ser	Glu	Ser	Ile	Gln	Ala	Leu	Gly	Trp	Val	Ala	130	135	140
Leu	Ala	Ala	Lys	Pro	Gly	Pro	Phe	Val	Lys	Glu	Met	Asn	Asp	Ala	Ala	145	150	155
Met	Phe	Tyr	Thr	Asn	Arg	Val	Leu	Lys	Glu	Tyr	Arg	Asp	Val	Asp	Lys	165	170	175
Lys	His	Val	Asp	Trp	Val	Arg	Ala	Tyr	Leu	Ser	Ile	Trp	Thr	Glu	Leu	180	185	190
Gln	Ala	Tyr	Ile	Lys	Glu	Phe	His	Thr	Thr	Gly	Leu	Ala	Trp	Ser	Lys	195	200	205
Thr	Gly	Pro	Val	Ala	Lys	Glu	Leu	Ser	Gly	Leu	Pro	Ser	Gly	Pro	Ser	210	215	220
Val	Gly	Ser	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Pro	Pro	Pro	Pro	Pro	225	230	235
Ile	Pro	Thr	Ser	Ser	Gly	Ser	Asp	Asp	Ser	Ala	Ser	Arg	Ser	Ala	Leu	245	250	255
Phe	Ala	Gln	Ile	Asn	Gln	Gly	Glu	Ser	Ile	Thr	His	Ala	Leu	Lys	His	260	265	270
Val	Ser	Asp	Asp	Met	Lys	Thr	His	Lys	Asn	Pro	Ala	Leu	Lys	Ala	Gln	275	280	285
Ser	Gly	Pro	Val	Arg	Ser	Gly	Pro	Lys	Pro	Phe	Ser	Ala	Pro	Lys	Pro	290	295	300
Gln	Thr	Ser	Pro	Ser	Pro	Lys	Pro	Ala	Thr	Lys	Lys	Glu	Pro	Ala	Leu	305	310	315
Leu	Glu	Leu	Glu	Gly	Lys	Lys	Trp	Arg	Val	Glu	Asn	Gln	Glu	Asn	Val	325	330	335
Ser	Asn	Leu	Val	Ile	Asp	Asp	Thr	Glu	Leu	Lys	Gln	Val	Ala	Tyr	Ile	340	345	350

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Tyr Lys Cys Val Asn Thr Thr Leu Gln Ile Lys Gly Lys Ile Asn Ser
355 360 365

Ile Thr Val Asp Asn Cys Lys Lys Leu Gly Leu Val Phe Asp Asp Val
370 375 380

Val Gly Ile Val Glu Ile Ile Asn Ser Arg Asp Val Lys Val Gln Val
385 390 395 400

Met Gly Lys Val Pro Thr Ile Ser Ile Asn Lys Thr Asp Gly Cys His
405 410 415

Ala Tyr Leu Ser Lys Asn Ser Leu Asp Cys Glu Ile Val Ser Ala Lys
420 425 430

Ser Ser Glu Met Asn Val Leu Ile Pro Thr Glu Gly Gly Asp Phe Asn
435 440 445

Glu Phe Pro Val Pro Glu Gln Phe Lys Thr Leu Trp Asn Gly Gln Lys
450 455 460

Leu Val Thr Thr Val Thr Glu Ile Ala Gly
465 470

<210> 19
<211> 475
<212> PRT
<213> Homo sapiens

<400> 19

Met Ala Asp Met Gln Asn Leu Val Glu Arg Leu Glu Arg Ala Val Gly
1 5 10 15

Arg Leu Glu Ala Val Ser His Thr Ser Asp Met His Arg Gly Tyr Ala
20 25 30

Asp Ser Pro Ser Lys Ala Gly Ala Ala Pro Tyr Val Gln Ala Phe Asp
35 40 45

Ser Leu Leu Ala Gly Pro Val Ala Glu Tyr Leu Lys Ile Ser Lys Glu
50 55 60

Ile Gly Gly Asp Val Gln Lys His Ala Glu Met Val His Thr Gly Leu
65 70 75 80

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Lys Leu Glu Arg Ala Leu Leu Val Thr Ala Ser Gln Cys Gln Gln Pro
85 90 95

Ala Glu Asn Lys Leu Ser Asp Leu Leu Ala Pro Ile Ser Glu Gln Ile
100 105 110

Lys Glu Val Ile Thr Phe Arg Glu Lys Asn Arg Gly Ser Lys Leu Phe
115 120 125

Asn His Leu Ser Ala Val Ser Glu Ser Ile Gln Ala Leu Gly Trp Val
130 135 140

Ala Met Ala Pro Lys Pro Gly Pro Tyr Val Lys Glu Met Asn Asp Ala
145 150 155 160

Ala Met Phe Tyr Thr Asn Arg Val Leu Lys Glu Tyr Lys Asp Val Asp
165 170 175

Lys Lys His Val Asp Trp Val Lys Ala Tyr Leu Ser Ile Trp Thr Glu
180 185 190

Leu Gln Ala Tyr Ile Lys Glu Phe His Thr Thr Gly Leu Ala Trp Ser
195 200 205

Lys Thr Gly Pro Val Ala Lys Glu Leu Ser Gly Leu Pro Ser Gly Pro
210 215 220

Ser Ala Gly Ser Gly Pro Pro Pro Pro Pro Gly Pro Pro Pro Pro
225 230 235 240

Pro Val Ser Thr Ser Ser Gly Ser Asp Glu Ser Ala Ser Arg Ser Ala
245 250 255

Leu Phe Ala Gln Ile Asn Gln Gly Glu Ser Ile Thr His Ala Leu Lys
260 265 270

His Val Ser Asp Asp Met Lys Thr His Lys Asn Pro Ala Leu Lys Ala
275 280 285

Gln Ser Gly Pro Val Arg Ser Gly Pro Lys Pro Phe Ser Ala Pro Lys
290 295 300

Pro Gln Thr Ser Pro Ser Pro Lys Arg Ala Thr Lys Lys Glu Pro Ala
305 310 315 320

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Val Leu Glu Leu Glu Gly Lys Lys Trp Arg Val Glu Asn Gln Glu Asn
325 330 335

Val Ser Asn Leu Val Ile Glu Asp Thr Glu Leu Lys Gln Val Ala Tyr
340 345 350

Ile Tyr Lys Cys Val Asn Thr Thr Leu Gln Ile Lys Gly Lys Ile Asn
355 360 365

Ser Ile Thr Val Asp Asn Cys Lys Lys Leu Gly Leu Val Phe Asp Asp
370 375 380

Val Val Gly Ile Val Glu Ile Ile Asn Ser Lys Asp Val Lys Val Gln
385 390 395 400

Val Met Gly Lys Val Pro Thr Ile Ser Ile Asn Lys Thr Asp Gly Cys
405 410 415

His Ala Tyr Leu Ser Lys Asn Ser Leu Asp Cys Glu Ile Val Ser Ala
420 425 430

Lys Ser Ser Glu Met Asn Val Leu Ile Pro Thr Glu Gly Gly Asp Phe
435 440 445

Asn Glu Phe Pro Val Pro Glu Gln Phe Lys Thr Leu Trp Asn Gly Gln
450 455 460

Lys Leu Val Thr Thr Val Thr Glu Ile Ala Gly
465 470 475

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 20

ccattttcca agaggaagca

20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 21
ccgacactgc atttgcttta 20

<210> 22
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 22
actttcgatg gtaggatag 19

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 23
tgatcatctt cgatccccta 20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 24
atgtcaaccg aggagagtca 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 25
atgtacgaga ttggtgtagg 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 26
agtgaaaatc catctccagc 20

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 27
ccagcatggt caacaatttg ag 22

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequenceq

<220>
<223> Synthetic oligonucleotide

<400> 28
ggagttgaaa gtggtttggt caatac 26

<210> 29
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 29
ggctggtaga gacttgacca accatttg 28